

ABSTRACT OF THE DISCLOSURE

Methods and reagents are disclosed which provide for more sensitive, more accurate and higher through-put analyses of target nucleic acid sequences. The methods and reagents of the present invention may be generically applied to generally any target nucleic acid sequence and do not require *a priori* information about the presence, location or identity of mutations in the target nucleic acid sequence. The reagents of the invention are mixtures of oligonucleotide precursors having a high level of coverage and mass number complexity, and also having tags analyzable by mass spectrometry which are covalently linked to the precursors through cleavable bonds. A method is also disclosed for analyzing a target nucleic acid sequence employing the mixtures of oligonucleotide precursors having tags analyzable by mass spectrometry covalently linked to the oligonucleotide precursors through cleavable bonds, and chemical or enzymatic assays to alter the mass of the oligonucleotide precursors prior to mass spectral analysis. The enzymatic assay may be a polymerase extension assay or a ligation-based assay. The kits for carrying out the methods of the invention are also disclosed.

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